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SEQUENCE LISTING

<110> Julius-Maximilians-Universität Würzburg

<120> Millisecond activation switch for seven-transmembrane proteins

<130> H1340 PCT S3

<150> DE 102 59 874.6

<151> 2002-12-19

<150> EP 03 00 4394.7

<151> 2003-03-03

<160> 46

<170> PatentIn version 3.1

<210> 1

<211> 1409

<212> DNA

<213> Mouse

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Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
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Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
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Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
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Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
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Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
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Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
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Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
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Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
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Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
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Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
210 215 220

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly
245 250 255

Gly Ala Asp Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly
260 265 270

Pro Thr Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala
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Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp
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Leu Glu Glu Ser Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro
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Arg Arg Pro Asp Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser
325 330 335

Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala
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Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly
355 360 365

Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe
370 375 380

Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe

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 35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
 50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
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Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
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Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

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105

110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
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Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
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Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
 145 150 155 160

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
 165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
 180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
 195 200 205

Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
 210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
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Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
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Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
 260 265 270

Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
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Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
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Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
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Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
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Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
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Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
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Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu
 405 410 415

Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val
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Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
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Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
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Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
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Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
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Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 515 520 525

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
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Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 545 550 555 560

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
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Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala
 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
 50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
 65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
 85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
 100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
 115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
 130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
 145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
 165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met
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Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys
 195 200 205

Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu

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210

215

220

Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly Leu
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Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr Phe
 245 250 255

Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu Ala
 260 265 270

Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala
 275 280 285

Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser
 290 295 300

His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala
 305 310 315 320

Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg
 325 330 335

Leu Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His
 340 345 350

Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly
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Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu
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Leu Ser His Glu Leu Lys Gly
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35          40          45

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65          70          75          80

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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100         105         110

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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
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Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

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165

170

175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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cgcacaaagg ccatcattgt caccgtgtgg gtcacatcgg ctgtcatctc cttcccgcca      540
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ggggtggtgc ccatcctggc cgagctggac ggcgacgtaa acggccacaa gttcagcgtg      840
tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt catctgcacc      900
accggcaagc tgcccgtgcc ctggcccacc ctctgaccca ccttcggcta cggcctgcag      960

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15/66

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 aacatcgagg acggcagcgt gcagctcgcc gaccactacc agcagaacac ccccatcggc 1320
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<210> 12

<211> 818

<212> PRT

<213> artificial sequence

<220>

<223> alpha 2a adrenergic receptor-cam "chameleon" amino acid sequence

16/66

<400> 12

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Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly
 20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
 35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
 50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
 65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
 100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
 115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
 130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
 145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
 180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
 195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
 210 215 220

17/66

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Met Val Ser Lys Gly Glu
245 250 255

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
260 265 270

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
275 280 285

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
290 295 300

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln
305 310 315 320

Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
325 330 335

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
340 345 350

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
355 360 365

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
370 375 380

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
385 390 395 400

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
405 410 415

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
420 425 430

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
435 440 445

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
450 455 460

18/66

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
 465 470 475 480

Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Trp Arg Gly Arg Gln Asn
 485 490 495

Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe
 500 505 510

Val Val Cys Trp Phe Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val
 515 520 525

Gly Cys Pro Val Pro Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly
 530 535 540

Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His
 545 550 555 560

Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys
 565 570 575

Arg Ile Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 580 585 590

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 595 600 605

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 610 615 620

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 625 630 635 640

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 645 650 655

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 660 665 670

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 675 680 685

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 690 695 700

19/66

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
705 710 715 720

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
725 730 735

Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
740 745 750

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
755 760 765

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
770 775 780

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
785 790 795 800

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
805 810 815

Tyr Lys

<210> 13
<211> 2928
<212> DNA
<213> artificial sequence

<220>
<223> PTH receptor-cam "chameleon" 8 cDNA sequence

<400> 13
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ctgcaccgtg ctcaggccca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc 180
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agcaggtacc gagggcgccc ctgtctgccc gaatgggacc acatcctgtg ctggccgctg 360
ggggcaccag gtgaggtggt ggctgtgccc tgtccggact acatttatga cttcaatcac 420
aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac 480

20/66

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cgggaggtgt ttgaccgcct gggcatgatt tacaccgtgg gctactccgt gtccctggcg	600
tccctcaccg tagctgtgct catcctggcc tacttttaggc ggctgcactg cacgcgcaac	660
tacatccaca tgcacctgtt cctgtccttc atgtgcgcgc ccgtgagcat cttcgtcaag	720
gacgctgtgc tctactctgg cgccacgctt gatgaggctg agcgccctcac cgaggaggag	780
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tgcagggttg ctgtgacctt cttccttttac ttcttgcca ccaactacta ctggattctg	900
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tccgccctga gcaaagacct caacgagaag cgcatcaca tggctcctgct ggagttcgtg	1860
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attgtcttca tggccacacc atacaccgag gtctcaggga cgctctggca agtccagatg	2040
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21/66

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gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacia gctggagtac 2640
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cagtcgccc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc 2880
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<210> 14

<211> 975

<212> PRT

<213> artificial sequence

<220>

<223> PTH receptor-cam8 "chameleon" amino acid sequence

<400> 14

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Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
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```

```

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
          20           25           30

```

```

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
          35           40           45

```

```

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
          50           55           60

```

```

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
65           70           75           80

```

```

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
          85           90           95

```

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Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

```

22/66

100	105	110
Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala 115 120 125		
Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala 130 135 140		
Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His 145 150 155 160		
Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn 165 170 175		
Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr 180 185 190		
Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile 195 200 205		
Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met 210 215 220		
His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys 225 230 235 240		
Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu 245 250 255		
Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala 260 265 270		
Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe 275 280 285		
Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu 290 295 300		
Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr 305 310 315 320		
Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val 325 330 335		

23/66

Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
 340 345 350

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
 355 360 365

Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
 370 375 380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Met Val Ser Lys Gly
 385 390 395 400

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
 405 410 415

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
 420 425 430

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
 435 440 445

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val
 450 455 460

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
 465 470 475 480

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 485 490 495

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 500 505 510

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 515 520 525

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
 530 535 540

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
 545 550 555 560

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 565 570 575

24/66

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 580 585 590

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 595 600 605

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 610 615 620

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Cys Asp Thr Arg Gln
 625 630 635 640

Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
 645 650 655

Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
 660 665 670

Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
 675 680 685

Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu
 690 695 700

Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu
 705 710 715 720

Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
 725 730 735

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 740 745 750

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 755 760 765

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 770 775 780

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 785 790 795 800

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 805 810 815

25/66

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
820 825 830

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
835 840 845

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
850 855 860

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
865 870 875 880

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
885 890 895

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
900 905 910

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
915 920 925

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
930 935 940

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
945 950 955 960

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
965 970 975

<210> 15

<211> 2361

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 cDNA sequence; A2A "chameleon"

<400> 15

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accaactact ttgtggtgtc actggcgggcg gccgacatcg cagtgggtgt gctcgccatc 180

ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240

26/66

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27/66

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<210> 16
 <211> 784
 <212> PRT
 <213> artificial sequence

<220>
 <223> A2A-CFP14/10-YFP-C33 amino acid sequence; "A2A chameleon"
 <400> 16

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
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Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala
 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
 50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
 65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
 85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
 100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
 115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
 130 135 140

28/66

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
 145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
 165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met
 180 185 190

Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys
 195 200 205

Gln Met Glu Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 210 215 220

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 225 230 235 240

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 245 250 255

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 260 265 270

Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
 275 280 285

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 290 295 300

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 305 310 315 320

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 325 330 335

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 340 345 350

Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 355 360 365

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 370 375 380

29/66

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 385 390 395 400

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 405 410 415

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 420 425 430

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 435 440 445

Lys Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val
 450 455 460

Gly Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe
 465 470 475 480

Thr Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr
 485 490 495

Leu Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile
 500 505 510

Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile
 515 520 525

Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr
 530 535 540

Ser Ala Arg Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 545 550 555 560

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 565 570 575

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 580 585 590

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 595 600 605

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro

30/66

610

615

620

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 625 630 635 640

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 645 650 655

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 660 665 670

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 675 680 685

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 690 695 700

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 705 710 715 720

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 725 730 735

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
 740 745 750

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 755 760 765

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
 770 775 780

<210> 17

<211> 477

<212> DNA

<213> Mouse

<400> 17

gtgcgtatatt accagatcgc caagcgtcgc acccgcgtgc ctcccagccg ccgggggtccg 60

gacgcctggt cgcgcgcgcc ggggggcgcc gatcgcaggc ccaacgggct gggcccggag 120

cgcgggcgcg gtccacggg cgctgaggcg gagccgctgc ccaccagct taacgggtgcc 180

ccggggggagc ccgcgcccgc cgggccccgc gatggggatg cgctggacct agaggagagt 240

tcgtcgtccg agcaagccga gcggccccgc gggccccgca gaccgaccg cggcccccca 300

31/66

gccaaagggca agaccgggc gagtcaggtg aagccggggg acagtctgcc gcggcgcggg 360
 cccggggccg cggggccggg ggcttcgggg tccgggcacg gagaggagcg cggcgggggc 420
 gccaaagcgt cgcgctggcg cgggaggcaa aaccgggaga aacgcttcac gttcgtg 477

<210> 18
 <211> 159
 <212> PRT
 <213> Mouse

<400> 18

Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg Val Pro Pro Ser
 1 5 10 15

Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly Gly Ala Asp Arg
 20 25 30

Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala
 35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro
 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser
 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp
 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro
 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala
 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser
 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val
 145 150 155

<210> 19
 <211> 63
 <212> DNA
 <213> Mouse

32/66

<400> 19
cacgacttcc gacgcgcctt caagaagatc ctctgccgtg gggacagaaa acgcatcgtg 60

tga 63

<210> 20
<211> 20
<212> PRT
<213> Mouse

<400> 20

His Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg
1 5 10 15

Lys Arg Ile Val
20

<210> 21
<211> 107
<212> DNA
<213> homo sapiens

<400> 21
ggatcttcct ggcggcgcgga cgacagctga agcagatgga gagccagcct ctgccggggg 60

agcgggcacg gtccacactg cagaaggagg tccatgctgc caagtca 107

<210> 22
<211> 36
<212> PRT
<213> homo sapiens

<400> 22

Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln
1 5 10 15

Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu Gln Lys Glu Val His
20 25 30

Ala Ala Lys Ser
35

<210> 23
<211> 369
<212> DNA
<213> homo sapiens

<400> 23
cgtatccgcg agttccgccg gaccttcgcg aagatcattc gcagccacgt cctgaggcag 60

33/66

caagaacctt tcaaggcagc tggcaccagt gcccggtct tggcagctca tggcagtgac 120
 ggagagcagg tcagcctccg tctcaacggc caccgccag gagtgtgggc caacggcagt 180
 gctccccacc ctgagcggag gcccaatggc tatgccctgg ggctggtgag tggagggagt 240
 gcccaagagt cccaggggaa cacgggcctc ccagacgtgg agctccttag ccatgagctc 300
 aaggagtggt gccagagacc ccctggccta gatgacccc tggcccagga tggagcagga 360
 gtgtcctga 369

<210> 24
 <211> 102
 <212> PRT
 <213> homo sapiens

<400> 24

Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His
 1 5 10 15

Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg
 20 25 30

Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu
 35 40 45

Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro
 50 55 60

Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser
 65 70 75 80

Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu
 85 90 95

Ser His Glu Leu Lys Gly
 100

<210> 25
 <211> 57
 <212> DNA
 <213> homo sapiens

<400> 25
 accaagctgc gggagaccaa cgccggccgg tgtgacacac ggcagcagta ccggaag 57

<210> 26
 <211> 19

34/66

<212> PRT
 <213> homo sapiens

<400> 26

Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln
 1 5 10 15

Tyr Arg Lys

<210> 27
 <211> 393
 <212> DNA
 <213> homo sapiens

<400> 27
 gaggtacaag ctgagatcaa gaaatcttgg agccgctgga cactggcact ggacttcaag 60
 cgaaaggcac gcagcgggag cagcagctat agctacggcc ccatggtgtc ccacacaagt 120
 gtgaccaatg tcggcccccg tgtgggactc ggccctgcccc tcagcccccg cctactgccc 180
 actgccacca ccaacggcca cctcagctg cctggccatg ccaagccagg gaccccagcc 240
 ctggagaccc tcgagaccac accacctgcc atggctgctc ccaaggacga tgggttcctc 300
 aacggctcct gctcaggcct ggacgaggag gcctctgggc ctgagcggcc acctgccttg 360
 ctacaggaag agtgggagac agtcatgtga tga 393

<210> 28
 <211> 129
 <212> PRT
 <213> homo sapiens

<400> 28

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
115 120 125

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<210> 29
<211> 264
<212> PRT
<213> artificial sequence
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<220>
<223> PTHR-cam7 amino acid sequence

<400> 29

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu
20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
65 70 75 80

Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys
				85					90					95	

Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
115 120 125

36/66

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys
 260

<210> 30

<211> 270

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam9 amino acid sequence

<400> 30

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met
 20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 35 40 45

37/66

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 180 185 190

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 195 200 205

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 210 215 220

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser
 225 230 235 240

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 245 250 255

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 260 265 270

<210> 31

<211> 272

<212> PRT

38/66

<213> artificial sequence

<220>

<223> PTHR-cam8 amino acid sequence

<400> 31

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 50 55 60

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met
 100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 195 200 205

39/66

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 260 265 270

<210> 32

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam2 amino acid sequence

<400> 32

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 35 40 45

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
 100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

40/66

130

135

140

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 145 150 155 160

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 165 170 175

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 180 185 190

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 195 200 205

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 210 215 220

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
 225 230 235 240

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 245 250 255

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
 260 265 270

Leu Tyr Lys
 275

<210> 33

<211> 289

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam5 amino acid sequence

<400> 33

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

41/66

Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 50 55 60

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 65 70 75 80

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 85 90 95

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 100 105 110

Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His
 115 120 125

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 130 135 140

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 145 150 155 160

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 165 170 175

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 180 185 190

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 195 200 205

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 210 215 220

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 225 230 235 240

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 245 250 255

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 260 265 270

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr

42/66

275

280

285

Lys

<210> 34

<211> 325

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-caml amino acid sequence

<400> 34

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
 85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg
 145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
 165 170 175

43/66

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 180 185 190

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 195 200 205

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 210 215 220

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 225 230 235 240

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
 245 250 255

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 260 265 270

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 275 280 285

Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 290 295 300

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
 305 310 315 320

Asp Glu Leu Tyr Lys
 325

<210> 35

<211> 339

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam4 amino acid sequence

<400> 35

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

44/66

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
100 105 110

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
115 120 125

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
130 135 140

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
145 150 155 160

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
165 170 175

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
180 185 190

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
195 200 205

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
210 215 220

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
225 230 235 240

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
245 250 255

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
260 265 270

45/66

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 275 280 285

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
 290 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 305 310 315 320

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
 325 330 335

Leu Tyr Lys

<210> 36
 <211> 354
 <212> PRT
 <213> artificial sequence

<220>
 <223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
 100 105 110

46/66

Gly Pro Glu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 115 120 125

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
 130 135 140

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 145 150 155 160

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 165 170 175

Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp
 180 185 190

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 195 200 205

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 210 215 220

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 225 230 235 240

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 245 250 255

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
 260 265 270

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 275 280 285

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 290 295 300

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 305 310 315 320

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 325 330 335

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 340 345 350

47/66

Tyr Lys

<210> 37

<211> 368

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-caml0 amino acid sequence

<400> 37

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
 100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
 115 120 125

Met Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 130 135 140

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 145 150 155 160

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 165 170 175

48/66

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 180 185 190

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met
 195 200 205

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 210 215 220

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 225 230 235 240

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 245 250 255

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 260 265 270

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38

49/66

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Glu Leu
 20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
 35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
 85 90 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
 100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
 115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
 130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
 145 150 155 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
 165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
 180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 195 200 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 225 230 235 240

50/66

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
 245 250 255

Gly Met Asp Glu Leu Tyr Lys Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
 260 265 270

Pro Met Val Ser His Thr Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 275 280 285

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 290 295 300

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 305 310 315 320

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 325 330 335

Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser
 340 345 350

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 355 360 365

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 370 375 380

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 385 390 395 400

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 405 410 415

Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile
 420 425 430

Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg
 435 440 445

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 450 455 460

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 465 470 475 480

51/66

Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 485 490 495

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly
 500 505 510

Met Asp Glu Leu Tyr Lys
 515

<210> 39
 <211> 1737
 <212> DNA
 <213> artificial sequence

<220>
 <223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39
 atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc 60
 atcctgggca atgtgctggc gtgctgggcc gtgtggctca acagcaacct gcagaacgct 120
 accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc 180
 ccctttgccca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240
 gcctgcttcg tcctggtcct cagcagagc tccatcttca gtctcctggc catcgccatt 300
 gaccgctaca ttgccatccg catcccgctc cggtaacaatg gcttggtgac cgggacgagg 360
 gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg 420
 ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg 480
 gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc 540
 aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc 600
 ttcttggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt 660
 gcacgggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg 720
 ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc 780
 gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840
 tcggttgtga atcccttcat ctacgcctac cgtatccgag agttccgcca gaccttccgc 900
 aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt 960
 gcccggtctt tggcagctca tggcagtgc ggagagcagg tcagcctccg tctcaacggt 1020
 gtgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctggtcga gctggacggc 1080

52/66

gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 1140
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 1200
 gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260
 cacgacttct tcaagtccgc catgcccga ggtacgtcc aggagcgtac catcttcttc 1320
 aaggacgacg gcaactacaa gaccgcgcgc gaggtgaagt tcgagggcga caccctgggtg 1380
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440
 ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500
 atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560
 cactaccagc agaacacccc catcgggcgc ggccccgtgc tgctgcccga caaccactac 1620
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680
 ctggagttcg tgaccgcgcg cgggatcact ctcggcacatg acgagctgta caagtaa 1737

<210> 40
 <211> 578
 <212> PRT
 <213> artificial sequence

<220>
 <223> A2A-FlashPG-CFP-C49 amino acid sequence

<400> 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

53/66

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
 130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
 195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
 325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val

54/66

340

345

350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
 465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
 485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
 500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 565 570 575

55/66

Tyr Lys

<210> 41

<211> 1686

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 cDNA sequence

<400> 41

```

atgcccataca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc      60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc      120
accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc      180
ccctttgcc a tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt      240
gcctgcttcg tcctggtcct cagcgagagc tccatcttca gtctcctggc catcgccatt      300
gaccgctaca ttgccatccg catcccgctc cgggtacaatg gcttggtgac cgggacgagg      360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg      420
ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg      480
gagggccaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc      540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc      600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt      660
gcacgggtcca cactgcagaa ggagggtccat gctgccaaagt cactggccat cattgtgggg      720
ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc      780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat      840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc      900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt      960
gcccggttcg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag     1020
ctggacggcg acgtaaacgg ccacagggtc agcgtgtccg gcgagggcga gggcgatgcc     1080
acctacggca agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg     1140
cccaccctcg tgaccaccct gacctggggc gtgcagtgtc tcagccgcta ccccgaccac     1200
atgaagcagc acgacttctt caagtccgcc atgccgaag gctacgtcca ggagcgtacc     1260
atcttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac     1320
accctggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg     1380

```

56/66

```

gggcacaagc tggagtacaa ctacatcagc cacaacgtct atatcaccgc cgacaagcag 1440
aagaacggca tcaaggccca cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag 1500
ctcgccgacc actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccagc 1560
aaccactacc tgagcaccca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac 1620
atggtcctgc tggagttcgt gaccgcccgc gggatcactc tcggcatgga cgagctgtac 1680
aagtaa 1686

```

```

<210> 42
<211> 561
<212> PRT
<213> artificial sequence

<220>
<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

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```

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1           5           10           15

```

```

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
          20           25           30

```

```

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
          35           40           45

```

```

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
          50           55           60

```

```

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65           70           75           80

```

```

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
          85           90           95

```

```

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
          100          105          110

```

```

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
          115          120          125

```

```

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
          130          135          140

```


57/66

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
 195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
 305 310 315 320

Ala Arg Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 325 330 335

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val
 340 345 350

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 355 360 365

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 370 375 380

58/66

Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His
385 390 395 400

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
405 410 415

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
420 425 430

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
435 440 445

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
450 455 460

Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
465 470 475 480

Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp
485 490 495

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
500 505 510

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
515 520 525

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
530 535 540

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
545 550 555 560

Lys

<210> 43

<211> 1788

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP-ModelPG-C49 cDNA sequence

<400> 43

atgcccatca tgggctcctc ggtgtacatc acgggtggagc tggccattgc tgtgctggcc

60

59/66

atcctgggca atgtgctggt gtgctgggcc gtgtggetca acagcaacct gcagaacgtc	120
accaactact ttgtgggtgc actggcgggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc a tcaccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcctgggtcct cagcgagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgctc cgggtacaatg gcttgggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttga acaactgcg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agcctctgcc gggggagcgg	660
gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720
ctctttgccc tctgctggct gccctacac atcatcaact gcttcacttt cttctgcccc	780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat	840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc	900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt	960
gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggc	1020
gtgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctgggtcga gctggacggc	1080
gacgtaaacg gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctaaggc	1140
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc	1200
gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag	1260
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgtac catcttcttc	1320
aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctggtg	1380
aaccgcatcg agctgaagg catcgacttc aaggaggacg gcaacatcct ggggcacaag	1440
ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc	1500
atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac	1560
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac	1620
ctgagcacc agtccgcct gagcaaagac cccaacgaga agcgcgatca catggtcctg	1680
ctggagttcg tgaccgcgc cgggatcact ctcgcatgg acgagctgta caaggctgag	1740
gctgcagcgc gcgaagcatg ctgcccaggt tgttgcgctc gcgcatga	1788

60/66

<210> 44
<211> 595
<212> PRT
<213> artificial sequence

<220>
<223> A2A-CFP-ModelPG-C49 amino acid sequence

<400> 44

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

61/66

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
 195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
 325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
 370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
 420 425 430

62/66

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
 435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
 450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
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Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
 485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
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Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
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Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys
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Ala Arg Ala
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63/66

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64/66

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 35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
 100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
 130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
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Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
 195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
 210 215 220

65/66

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
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Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
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Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
 340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
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Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
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Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
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Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu

66/66

450

455

460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys

50/66

51/66